



1001066/1052302 # 9

SEQUENCE LISTING

<110> Afar, Daniel
Hubert, Rene S.
Leong, Kahan
Raitano, Arthur B.
Saffran, Douglas C.
Mitchell, Steve Chappell

<120> NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
EXPRESSED IN HUMAN CANCERS AND USES THEREOF

<130> 511582001601

<140> US 10/010,667

<141> 2001-12-06

<150> 09/323,873

<151> 1999-06-01

<150> 60/087,520

<151> 1998-06-01

<150> 60/091,183

<151> 1998-06-30

<160> 32

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<212> DNA

<213> Homo Sapiens

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aaagacctgt	gcttttgcat	ttgcaccaa	cagcccacgc	tgatgaattt	gactgccctt	240
cagaacttca	gcacacacag	gaactctttc	cacagtggca	cttgccaatt	aaaatagctg	300
ctattatagc	atctctgact	tttctttaca	ctcttctgag	ggaagtaatt	caccctttag	360
caacttccca	tcaacaatat	ttttataaaa	ttccaatcct	ggtcatcaac	aaagtcttgc	420
caatggtttc	catcactctc	ttggcattgg	tttacctgcc	aggtgtgata	gcagcaattg	480
tccaacttca	taatggaacc	aagtataaga	agtttccaca	ttggttggat	aagtggatgt	540
taacaagaaa	gcagtttggg	cttctcagtt	tcttttttgc	tgtactgcat	gcaatttata	600
gtctgtctta	cccaatgagg	cgatcctaca	gatacaagtt	gctaaactgg	gcataatcaac	660
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ttgtttccct	tctactgggc	acaatacacg	cttgattttt	tgccctggaat	aagtggatag	900
atataaaaca	atttgtatgg	tatacacctc	caacttttat	gatagctgtt	ttccttccaa	960
ttgttgtcct	gatattttaa	agcatactat	tcctgccatg	cttgaggaag	aagatactga	1020
agattagaca	tggttgggaa	gacgtcacca	aaattaacaa	aactgagata	tggtcccagt	1080
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1195

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<213> Homo sapiens
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Gly	Glu	Thr	Ser	Met	Leu	Lys	Arg	Pro	Val	Leu	Leu	His	Leu	His	Gln		
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Thr	Ala	His	Ala	Asp	Glu	Phe	Asp	Cys	Pro	Ser	Glu	Leu	Gln	His	Thr		
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Gln	Glu	Leu	Phe	Pro	Gln	Trp	His	Leu	Pro	Ile	Lys	Ile	Ala	Ala	Ile		
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Ile	Ala	Ser	Leu	Thr	Phe	Leu	Tyr	Thr	Leu	Leu	Arg	Glu	Val	Ile	His		
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Pro	Leu	Ala	Thr	Ser	His	Gln	Gln	Tyr	Phe	Tyr	Lys	Ile	Pro	Ile	Leu		
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Val	Tyr	Leu	Pro	Gly	Val	Ile	Ala	Ala	Ile	Val	Gln	Leu	His	Asn	Gly		
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Thr	Lys	Tyr	Lys	Lys	Phe	Pro	His	Trp	Leu	Asp	Lys	Trp	Met	Leu	Thr		
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Arg	Lys	Gln	Phe	Gly	Leu	Leu	Ser	Phe	Phe	Phe	Ala	Val	Leu	His	Ala		
			165					170						175			
Ile	Tyr	Ser	Leu	Ser	Tyr	Pro	Met	Arg	Arg	Ser	Tyr	Arg	Tyr	Lys	Leu		
			180					185					190				
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Ile	Glu	His	Asp	Val	Trp	Arg	Met	Glu	Ile	Tyr	Val	Ser	Leu	Gly	Ile		
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225					230					235				240			
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			260					265					270				
Ala	Trp	Asn	Lys	Trp	Ile	Asp	Ile	Lys	Gln	Phe	Val	Trp	Tyr	Thr	Pro		
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Pro	Thr	Phe	Met	Ile	Ala	Val	Phe	Leu	Pro	Ile	Val	Val	Leu	Ile	Phe		
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Ala Ala Tyr Gln Leu Tyr Tyr Gly Thr Lys Tyr Arg Arg Phe Pro Pro
          35          40          45
Trp Leu Glu Thr Trp Leu Gln Cys Arg Lys Gln Leu Gly Leu Leu Ser
 50          55          60
Phe Phe Phe Ala Met Val His Val Ala Tyr Ser Leu Cys Leu Pro Met
65          70          75          80
Arg Arg Ser Glu Arg Tyr Leu Phe Leu Asn Met Ala Tyr Gln Gln Val
          85          90          95
His Ala Asn Ile Glu Asn Ser Trp Asn Glu Glu Glu Val Trp Arg Ile
          100          105          110
Glu Met Tyr Ile Ser Phe Gly Ile Met Ser Leu Gly Leu Leu Ser Leu
          115          120          125
Leu Ala Val Thr Ser Ile Pro Ser Val Ser Asn Ala Leu Asn Trp Arg
          130          135          140
Glu Phe Ser Phe Ile Gln Ser Thr Leu Gly Tyr Val Ala Leu Leu Ile
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attactttgc tctccctagt ataccttgca ggtccttctgg cagctgctta tcaactttat      180
tacggcacca agtataggag atttccacct tgggttgaaa cctgggttaca gtgtagaaaa      240
cagcttgat tactaagttg tttcttcgct atgggtccatg ttgcctacag cctctgctta      300
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tgtgactgag tgttggccag tgagatgaag tctcctcaaa ggaaggcagc atgtgtcctt      180
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atcttgtgta	cagcccacac	cctgggtgtac	gggtgggaaga	gattcctcag	cccttcaa	240
ctcagatggt	atcttcctgc	agcctacgtg	ttagggctta	tcattccttg	cactgtgctg	300
gtgatcaagt	ttgtccta	catgccatgt	gtagacaaca	cccttacaag	gatccgccag	360
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gctggccctc	ggcacgttgt ccctgctggc cgtgacctca
ctgccgtcca	ttgcaaaactc 180
gctcaactgg	agggagttca gcttcgttca gtcctcactg
ggctttgtgg	ccntcgtgct 240
gagcacactn	cacacgctca cctacggctg gacccgcgcc
ttcgaggaga	gccgctacaa 300
gttctacctn	cctccacct tcacgntcac gctgctgggtg
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Lys Ile Pro Ile Leu Val
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